

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/103,287

DATE: 07/06/98
TIME: 14:24:28

INPUT SET: S27178.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Wallis, Nicola G.
6 Burnham, Martin K. R.
7
8 (ii) TITLE OF INVENTION: murc
9
10
11 (iii) NUMBER OF SEQUENCES: 6
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Dechert, Price & Rhoads
15 (B) STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
16 (C) CITY: Philadelphia
17 (D) STATE: PA
18 (E) COUNTRY: USA
19 (F) ZIP: 19103-2793
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: Windows 95
25 (D) SOFTWARE: FastSEQ for Windows Version 2.0b
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER:
29 (B) FILING DATE:
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 60/052,720
34 (B) FILING DATE: 03-JUL-1997
35
36
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Falk, Stephen T
39 (B) REGISTRATION NUMBER: 36,795
40 (C) REFERENCE/DOCKET NUMBER: GM10025
41
42
43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: 215-994-2488
45 (B) TELEFAX: 215-994-2222
46 (C) TELEX:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGTAAGG	AGTTTTATAT	AATGACACAC	TATCATTTTG	TCGGAATTAA	AGGTTCTGGC	60
ATGAGTTCAT	TAGCACAAAT	CATGCATGAT	TTAGGACATG	AAGTTCAAGG	ATCGGATATT	120
GAGAACTACG	TATTTACAGA	AGTTGCTCTT	AGAAATAAGG	GGATAAAAAAT	ATTACCATTT	180
GGTGCTAATA	ACATAAAAAGA	AGATATGGTA	GTTATACAAG	GTAATGCATT	CGCGAGTAGC	240
CATGAAGAAA	TAGTACGTGC	ACATCAATTG	AAATTAGATG	TTGTAAGTTA	TAATGATTTT	300
TTAGGACAGA	TTATTGATCA	ATATACTTCA	GTAGCTGTAA	CTGGTGCACA	TGGTAAAACT	360
TCTACAACAG	GTTTATTATC	ACATGTTATG	AATGGTGATA	AAAAGACTTC	ATTTTTAATT	420
GGTGATGGCA	CAGGTATGGG	ATTGCCTGAA	AGTGATTATT	TCGCTTTTGA	GGCATGTGAA	480
TATAGACGTC	ACTTTTTAAG	TTATAAACCT	GATTACGCAA	TTATGACAAA	TATTGATTTT	540
GATCATCCTG	ATTATTTCAA	AGATATTAAT	GATGTTTTTG	ATGCATTCCA	AGAAATGGCA	600
CATAATGTTA	AAAAAGGTAT	TATTGCTTGG	GGTGATGATG	AACATCTACG	TAAAAATTGAA	660
GCAGATGTTT	CAATTTATTA	CTATGGATTT	AAAGATTCGG	ATGACATTTA	TGCTCAAAAT	720
ATTCAAATTA	CGGATAAAGG	TACTGCTTTT	GATGTGTATG	TGGATGGTGA	GTTTTATGAT	780
CACTTCCTGT	CTCCACAATA	TGGTGACCAT	ACAGTTTTTA	ATGCATTAGC	TGTAATTGCG	840
ATTAGTTATT	TAGAGAAGCT	AGATGTTACA	AATATTAAAG	AAGCATTAGA	AACGTTTGGT	900
GGTGTTAAAC	GTCGTTTCAA	TGAAACTACA	ATTGCAAATC	AAGTTATTGT	AGATGATTAT	960
GCACACCATC	CAAGAGAAAT	TAGTGCTACA	ATTGACACAG	CACGAAAGAA	ATATCCACAT	1020
AAAGAAGTTG	TTGCAGTATT	TCAACCACAC	ACTTTCCTTA	GAACACAAGC	ATTTTTAAAT	1080
GAATTTGCAG	AAAGTTTATG	TAAAGCAGAT	CGTGATTCTT	TATGTGAAAT	TTTTGGCTCA	1140
ATTAGAGAAA	ATTCTGGCGC	ATTAACGATA	CAAGATTTAA	TTGATAAAAT	TGGAGGTGCA	1200
TCGTTTCATTA	ATGAAGATCT	TATTAATGTA	TTAGAACAAT	TTGATAATGC	TGTTGTTTTA	1260
TTTATGGGTG	CAGGTGATAT	TCAAAAATTA	CAAAATGCAT	ATTTAGATAA	ATTAGGCATG	1320
AAAAATGCGT	TTTAATATGT	TTATAATAGA	G			1351

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	His	Tyr	His	Phe	Val	Gly	Ile	Lys	Gly	Ser	Gly	Met	Ser	Ser
1				5					10					15	
Leu	Ala	Gln	Ile	Met	His	Asp	Leu	Gly	His	Glu	Val	Gln	Gly	Ser	Asp
		20					25					30			
Ile	Glu	Asn	Tyr	Val	Phe	Thr	Glu	Val	Ala	Leu	Arg	Asn	Lys	Gly	Ile

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100		35		40		45													
101	Lys	Ile	Leu	Pro	Phe	Gly	Ala	Asn	Asn	Ile	Lys	Glu	Asp	Met	Val	Val			
102		50					55					60							
103	Ile	Gln	Gly	Asn	Ala	Phe	Ala	Ser	Ser	His	Glu	Glu	Ile	Val	Arg	Ala			
104	65					70					75				80				
105	His	Gln	Leu	Lys	Leu	Asp	Val	Val	Ser	Tyr	Asn	Asp	Phe	Leu	Gly	Gln			
106					85					90				95					
107	Ile	Ile	Asp	Gln	Tyr	Thr	Ser	Val	Ala	Val	Thr	Gly	Ala	His	Gly	Lys			
108				100					105					110					
109	Thr	Ser	Thr	Thr	Gly	Leu	Leu	Ser	His	Val	Met	Asn	Gly	Asp	Lys	Lys			
110			115					120					125						
111	Thr	Ser	Phe	Leu	Ile	Gly	Asp	Gly	Thr	Gly	Met	Gly	Leu	Pro	Glu	Ser			
112		130				135					140								
113	Asp	Tyr	Phe	Ala	Phe	Glu	Ala	Cys	Glu	Tyr	Arg	Arg	His	Phe	Leu	Ser			
114	145					150					155				160				
115	Tyr	Lys	Pro	Asp	Tyr	Ala	Ile	Met	Thr	Asn	Ile	Asp	Phe	Asp	His	Pro			
116				165					170					175					
117	Asp	Tyr	Phe	Lys	Asp	Ile	Asn	Asp	Val	Phe	Asp	Ala	Phe	Gln	Glu	Met			
118				180				185					190						
119	Ala	His	Asn	Val	Lys	Lys	Gly	Ile	Ile	Ala	Trp	Gly	Asp	Asp	Glu	His			
120			195					200					205						
121	Leu	Arg	Lys	Ile	Glu	Ala	Asp	Val	Pro	Ile	Tyr	Tyr	Tyr	Gly	Phe	Lys			
122		210				215					220								
123	Asp	Ser	Asp	Asp	Ile	Tyr	Ala	Gln	Asn	Ile	Gln	Ile	Thr	Asp	Lys	Gly			
124	225					230					235				240				
125	Thr	Ala	Phe	Asp	Val	Tyr	Val	Asp	Gly	Glu	Phe	Tyr	Asp	His	Phe	Leu			
126				245					250					255					
127	Ser	Pro	Gln	Tyr	Gly	Asp	His	Thr	Val	Leu	Asn	Ala	Leu	Ala	Val	Ile			
128				260				265					270						
129	Ala	Ile	Ser	Tyr	Leu	Glu	Lys	Leu	Asp	Val	Thr	Asn	Ile	Lys	Glu	Ala			
130			275					280					285						
131	Leu	Glu	Thr	Phe	Gly	Gly	Val	Lys	Arg	Arg	Phe	Asn	Glu	Thr	Thr	Ile			
132		290				295					300								
133	Ala	Asn	Gln	Val	Ile	Val	Asp	Asp	Tyr	Ala	His	His	Pro	Arg	Glu	Ile			
134	305					310					315				320				
135	Ser	Ala	Thr	Ile	Asp	Thr	Ala	Arg	Lys	Lys	Tyr	Pro	His	Lys	Glu	Val			
136				325					330					335					
137	Val	Ala	Val	Phe	Gln	Pro	His	Thr	Phe	Ser	Arg	Thr	Gln	Ala	Phe	Leu			
138				340				345					350						
139	Asn	Glu	Phe	Ala	Glu	Ser	Leu	Cys	Lys	Ala	Asp	Arg	Val	Phe	Leu	Cys			
140			355				360					365							
141	Glu	Ile	Phe	Gly	Ser	Ile	Arg	Glu	Asn	Ser	Gly	Ala	Leu	Thr	Ile	Gln			
142		370				375					380								
143	Asp	Leu	Ile	Asp	Lys	Ile	Gly	Gly	Ala	Ser	Phe	Ile	Asn	Glu	Asp	Leu			
144	385					390					395				400				
145	Ile	Asn	Val	Leu	Glu	Gln	Phe	Asp	Asn	Ala	Val	Val	Leu	Phe	Met	Gly			
146				405					410				415						
147	Ala	Gly	Asp	Ile	Gln	Lys	Leu	Gln	Asn	Ala	Tyr	Leu	Asp	Lys	Leu	Gly			
148				420				425					430						
149	Met	Lys	Asn	Ala	Phe														
150				435															
151																			
152																			

(2) INFORMATION FOR SEQ ID NO:3:

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(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 660 base pairs

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(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

162

163 ATTTAAAGAT TCGGATGACA TTTATGCTCA AATATTTCAA ATTACGGATA AAGGTACTGC 60

164 TGTGATGTG TATGTGGATG GTGAGTTTTA TGATCACTTC CTGTCTCCAC AATATGGTGA 120

165 CCATACAGTT TTAAATGCAT TAGCTGTAAT TGCGATTAGT TATTTAGAGA AGCTAGATGT 180

166 TACAAATATT AAAGAAGCAT TAGAAACGTT TGGTGGTGT AAACGTCGTT TCAATGAAAC 240

167 TACAATTGCA AATCAAGTTA TTGTAGATGA TTATGCACAC CATCCAAGAG AAATTAGTGC 300

168 TACAATTGAC ACAGCACGAA AGAAATATCC ACATAAAGAA GTTGTTCGAG TATTTCAACC 360

169 ACACACTTTC TCTAGAACAC AAGCATTTTT AAATGAAATT GCAGAAAGTT TAAGTAAAGC 420

170 AGATCGTGTA TTCTTATGTG AAATTTTTTG ATCAATTAGA GAAAATACTG GCGCATTAAC 480

171 GATACAAGAT TTAATTGATA AAATTGAAGG TGCATCGTTA ATTAATGAAG ATTCTATTAA 540

172 TGTATTAGAA CAATTTGATA ATGCTGTTGT TTTATTTATG GGTGCAGGTG ATATTCAAAA 600

173 ATTACAAAAT GCATATTTAG ATAAATTAGG CATGAAAAAT GCGTTTAAAT ATGTTTATAA 660

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175

(2) INFORMATION FOR SEQ ID NO:4:

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(i) SEQUENCE CHARACTERISTICS:

178

(A) LENGTH: 215 amino acids

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(B) TYPE: amino acid

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(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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186 Phe Lys Asp Ser Asp Asp Ile Tyr Ala Gln Ile Phe Gln Ile Thr Asp

187 1 5 10 15

188 Lys Gly Thr Ala Val Asp Val Tyr Val Asp Gly Glu Phe Tyr Asp His

189 20 25 30

190 Phe Leu Ser Pro Gln Tyr Gly Asp His Thr Val Leu Asn Ala Leu Ala

191 35 40 45

192 Val Ile Ala Ile Ser Tyr Leu Glu Lys Leu Asp Val Thr Asn Ile Lys

193 50 55 60

194 Glu Ala Leu Glu Thr Phe Gly Gly Val Lys Arg Arg Phe Asn Glu Thr

195 65 70 75 80

196 Thr Ile Ala Asn Gln Val Ile Val Asp Asp Tyr Ala His His Pro Arg

197 85 90 95

198 Glu Ile Ser Ala Thr Ile Asp Thr Ala Arg Lys Lys Tyr Pro His Lys

199 100 105 110

200 Glu Val Val Ala Val Phe Gln Pro His Thr Phe Ser Arg Thr Gln Ala

201 115 120 125

202 Phe Leu Asn Glu Phe Ala Glu Ser Leu Ser Lys Ala Asp Arg Val Phe

203 130 135 140

204 Leu Cys Glu Ile Phe Gly Ser Ile Arg Glu Asn Thr Gly Ala Leu Thr

205 145 150 155 160

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206 Ile Gln Asp Leu Ile Asp Lys Ile Glu Gly Ala Ser Leu Ile Asn Glu
207 165 170 175
208 Asp Ser Ile Asn Val Leu Glu Gln Phe Asp Asn Ala Val Val Leu Phe
209 180 185 190
210 Met Gly Ala Gly Asp Ile Gln Lys Leu Gln Asn Ala Tyr Leu Asp Lys
211 195 200 205
212 Leu Gly Met Lys Asn Ala Phe
213 210 215
214

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTCATTAAT GAACGATGC

19

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTACAAATA TTAAAGAAG

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/103,287

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Line

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Original Text